

Amendment and Response

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Serial No.: 10/008,355

Confirmation No.: 4382

Filed: November 8, 2001

For: DIPEPTIDYLPEPTIDASES AND METHODS OF USE

polypeptide having an aliphatic or an aromatic residue as a substituent on the α -carbon atom of the second amino acid from the N-terminal end of the polypeptide.

40. (New) The isolated nucleic acid of claim 39 having a nucleotide sequence comprising SEQ ID NO:1.

41. (New) An isolated nucleic acid encoding a peptidase having dipeptidylpeptidase amidolytic activity;

wherein the dipeptidylpeptidase amidolytic activity is defined as activity for cleaving the peptide bond between the second and the third amino acids from the N-terminal end of a target polypeptide having an aliphatic or an aromatic residue as a substituent on the α -carbon atom of the second amino acid from the N-terminal end of the polypeptide;

wherein the peptidase comprises a catalytic domain for dipeptidylpeptidase amidolytic activity; and

wherein the catalytic domain comprises a sequence comprising residues 543 to 712 of SEQ ID NO:2.

42. (New) The isolated nucleic acid of claim 41, wherein the catalytic domain comprises a sequence comprising residues 540 to 712 of SEQ ID NO:2.

43. (New) The isolated nucleic acid of claim 42, wherein the catalytic domain comprises a sequence comprising residues 522 to 712 of SEQ ID NO:2.

44. (New) An isolated nucleic acid encoding a peptidase having dipeptidylpeptidase amidolytic activity;

wherein the dipeptidylpeptidase amidolytic activity is defined as activity for cleaving the peptide bond between the second and the third amino acids from the N-terminal end of a target

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polypeptide having an aliphatic or an aromatic residue as a substituent on the α -carbon atom of the second amino acid from the N-terminal end of the polypeptide;

wherein the peptidase comprises a catalytic domain for dipeptidylpeptidase amidolytic activity;

wherein the catalytic domain comprises the sequence TGGNSGSPVF (SEQ ID NO:25);

wherein the catalytic domain has a percentage amino acid identity of greater than 40% with SEQ ID NO:2; and

wherein the percentage amino acid identity is determined by placing the TGGNSGSPVF residues of the catalytic domain of the peptidase in register with residues 644-653 of SEQ ID NO:2.

45. (New) The isolated nucleic acid of claim 44, wherein the catalytic domain has a percentage amino acid identity of greater than 50% with SEQ ID NO:2.

46. (New) The isolated nucleic acid of claim 45, wherein the catalytic domain has a percentage amino acid identity of greater than 60% with SEQ ID NO:2.

47. (New) The isolated nucleic acid of claim 46, wherein the catalytic domain has a percentage amino acid identity of greater than 70% with SEQ ID NO:2.

48. (New) The isolated nucleic acid of claim 47, wherein the catalytic domain has a percentage amino acid identity of greater than 80% with SEQ ID NO:2.

49. (New) The isolated nucleic acid of claim 48, wherein the catalytic domain has a percentage amino acid identity of greater than 90% with SEQ ID NO:2.

50. (New) An isolated nucleic acid encoding a peptidase having dipeptidylpeptidase amidolytic activity;

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wherein the dipeptidylpeptidase amidolytic activity is defined as activity for cleaving the peptide bond between the second and third amino acids from the N-terminal end of a target polypeptide having an aliphatic or an aromatic residue as a substituent on the α -carbon atom of the second amino acid from the N-terminal end of the polypeptide; and

wherein the nucleic acid comprises a nucleotide sequence having at least about 70% identity with SEQ ID NO:1.

51. (New) The isolated nucleic acid of claim 50, wherein the nucleic acid comprises a nucleotide sequence having at least about 80% identity with SEQ ID NO:1.

52. (New) The isolated nucleic acid of claim 51, wherein the nucleic acid comprises a nucleotide sequence having at least about 90% identity with SEQ ID NO:1.

53. (New) The isolated nucleic acid of claim 52, wherein the nucleic acid comprises a nucleotide sequence having at least about 95% identity with SEQ ID NO:1.